



SEQUENCE LISTING

<110> The University of British Columbia

<120> CADHERIN-11 EXPRESSION, AN ASSAY AND TREATMENT FOR CELLULAR
INVASIVENESS

<130> 80021-275

<140> PCT/CA99/01057

<141> 1999-10-29

<150> US 60/106,258

<151> 1998-10-30

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

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<212> DNA

<213> Homo sapiens

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<223> Description of Artificial Sequence: Sense
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Pro Ser Phe His Gly His His Glu Lys Gly Lys Glu Gly Gln Val Leu
35 40 45

Gln Arg Ser Lys Arg Gly Trp Val Trp Asn Gln Phe Phe Val Ile Glu
50 55 60

Glu Tyr Thr Gly Pro Asp Pro Val Leu Val Gly Arg Leu His Ser Asp
65 70 75 80

Ile Asp Ser Gly Asp Gly Asn Ile Lys Tyr Ile Leu Ser Gly Glu Gly
85 90 95

Ala Gly Thr Ile Phe Val Ile Asp Asp Lys Ser Gly Asn Ile His Ala
100 105 110

Thr Lys Thr Leu Asp Arg Glu Glu Arg Ala Gln Tyr Thr Leu Met Ala
115 120 125

Gln Ala Val Asp Arg Asp Thr Asn Arg Pro Leu Glu Pro Pro Ser Glu
130 135 140

Phe Ile Val Lys Val Gln Asp Ile Asn Asp Asn Pro Pro Glu Phe Leu
145 150 155 160

His Glu Thr Tyr His Ala Asn Val Pro Glu Arg Ser Asn Val Gly Thr
165 170 175

Ser Val Ile Gln Val Thr Ala Ser Asp Ala Asp Asp Pro Thr Tyr Gly
180 185 190

Asn Ser Ala Lys Leu Val Tyr Ser Ile Leu Glu Gly Gln Pro Tyr Phe
195 200 205

Ser Val Glu Ala Gln Thr Gly Ile Ile Arg Thr Ala Leu Pro Asn Met
 210 215 220

Asp Arg Glu Ala Lys Glu Glu Tyr His Val Val Ile Gln Ala Lys Asp
 225 230 235 240

Met Gly Gly His Met Gly Gly Leu Ser Gly Thr Thr Lys Val Thr Ile
 245 250 255

Thr Leu Thr Asp Val Asn Asp Asn Pro Pro Lys Phe Pro Gln Arg Leu
 260 265 270

Tyr Gln Met Ser Val Ser Glu Ala Ala Val Pro Gly Glu Glu Val Gly
 275 280 285

Arg Val Lys Ala Lys Asp Pro Asp Ile Gly Glu Asn Gly Leu Val Thr
 290 295 300

Tyr Asn Ile Val Asp Gly Asp Gly Met Glu Ser Phe Glu Ile Thr Thr
 305 310 315 320

Asp Tyr Glu Thr Gln Glu Gly Val Ile Lys Leu Lys Lys Pro Val Asp
 325 330 335

Phe Glu Thr Glu Arg Ala Tyr Ser Leu Lys Val Glu Ala Ala Asn Val
 340 345 350

His Ile Asp Pro Lys Phe Ile Ser Asn Gly Pro Phe Lys Asp Thr Val
 355 360 365

Thr Val Lys Ile Ser Val Glu Asp Ala Asp Glu Pro Pro Met Phe Leu
 370 375 380

Ala Pro Ser Tyr Ile His Glu Val Gln Glu Asn Ala Ala Ala Gly Thr
 385 390 395 400

Val Val Gly Arg Val His Ala Lys Asp Pro Asp Ala Ala Asn Ser Pro
 405 410 415

Ile Arg Tyr Ser Ile Asp Arg His Thr Asp Leu Asp Arg Phe Phe Thr
 420 425 430

Ile Asn Pro Glu Asp Gly Phe Ile Lys Thr Thr Lys Pro Leu Asp Arg
 435 440 445

Glu Glu Thr Ala Trp Leu Asn Ile Thr Val Phe Ala Ala Glu Ile His
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Asn Arg His Gln Glu Ala Gln Val Pro Val Ala Ile Arg Val Leu Asp
 465 470 475 480

Val Asn Asp Asn Ala Pro Lys Phe Ala Ala Pro Tyr Glu Gly Phe Ile
 485 490 495

Cys Glu Ser Asp Gln Thr Lys Pro Leu Ser Asn Gln Pro Ile Val Thr
 500 505 510

Ile Ser Ala Asp Asp Lys Asp Asp Thr Ala Asn Gly Pro Arg Phe Ile
 515 520 525

Phe Ser Leu Pro Pro Glu Ile Ile His Asn Pro Asn Phe Thr Val Arg
 530 535 540

Asp Asn Arg Asp Asn Thr Ala Gly Val Tyr Ala Arg Arg Gly Gly Phe
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Ser Arg Gln Lys Gln Asp Leu Tyr Leu Leu Pro Ile Val Ile Ser Asp
 565 570 575

Gly Gly Ile Pro Pro Met Ser Ser Thr Asn Thr Leu Thr Ile Lys Val
 580 585 590

Cys Gly Cys Asp Val Asn Gly Ala Leu Leu Ser Cys Asn Ala Glu Ala
 595 600 605

Tyr Ile Leu Asn Ala Gly Leu Ser Thr Gly Ala Leu Ile Ala Ile Leu
 610 615 620

Ala Cys Ile Val Ile Leu Leu Val Ile Val Val Leu Phe Val Thr Leu
 625 630 635 640

Arg Arg Gln Lys Lys Glu Pro Leu Ile Val Phe Glu Glu Glu Asp Val
 645 650 655

Arg Glu Asn Ile Ile Thr Tyr Asp Asp Glu Gly Gly Gly Glu Glu Asp
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Thr Glu Ala Phe Asp Ile Ala Thr Leu Gln Asn Pro Asp Gly Ile Asn
 675 680 685

Gly Phe Ile Pro Arg Lys Asp Ile Lys Pro Glu Tyr Gln Tyr Met Pro
 690 695 700

Arg Pro Gly Leu Arg Pro Ala Pro Asn Ser Val Asp Val Asp Asp Phe
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Ile Asn Thr Arg Ile Gln Glu Ala Asp Asn Asp Pro Thr Ala Pro Pro
725 730 735

Tyr Asp Ser Ile Gln Ile Tyr Gly Tyr Glu Gly Arg Gly Ser Val Ala
740 745 750

Gly Ser Leu Ser Ser Leu Glu Ser Ala Thr Thr Asp Ser Asp Leu Asp
755 760 765

Tyr Asp Tyr Leu Gln Asn Trp Gly Pro Arg Phe Lys Lys Leu Ala Asp
770 775 780

Leu Tyr Gly Ser Lys Asp Thr Phe Asp Asp Asp Ser
785 790 795